

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/519,812

Source: P4/10

Date Processed by STIC: 1/12/05

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PCT

## RAW SEQUENCE LISTING

DATE: 01/12/2005

PATENT APPLICATION: US/10/519,812

TIME: 10:05:30

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\01122005\J519812.raw

3 &lt;110&gt; APPLICANT: Byrne, Barry J.

4 Mah, Cathryn S.

6 &lt;120&gt; TITLE OF INVENTION: rAAV COMPOSITIONS AND METHODS FOR DELIVERY OF HUMAN FACTOR

VII

7 POLYPEPTIDES AND TREATMENT OF HEMOPHILIA A

9 &lt;130&gt; FILE REFERENCE: 4300.014300

C--&gt; 11 &lt;140&gt; CURRENT APPLICATION NUMBER: US/10/519,812

12 &lt;141&gt; CURRENT FILING DATE: 2004-12-28

14 &lt;150&gt; PRIOR APPLICATION NUMBER: PCT/US03/20756

15 &lt;151&gt; PRIOR FILING DATE: 2003-06-30

17 &lt;150&gt; PRIOR APPLICATION NUMBER: 60/392,725

18 &lt;151&gt; PRIOR FILING DATE: 2002-06-28

20 &lt;160&gt; NUMBER OF SEQ ID NOS: 17

22 &lt;170&gt; SOFTWARE: PatentIn version 3.2

24 &lt;210&gt; SEQ ID NO: 1

25 &lt;211&gt; LENGTH: 1440

26 &lt;212&gt; TYPE: DNA

27 &lt;213&gt; ORGANISM: Homo sapiens

29 &lt;400&gt; SEQUENCE: 1

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34 gaggagaaac acgggacatg ccgtggaagc cggggcctca cagagtcttc gtaaccagg      180
36 aggaagccca cggcgtcctg caccggcgcc ggcgcgccaa cgcgttctct gaggagctgc     240
38 ggccgggctc cctggagagg gagtgaagg aggagcagtg ctcttctcag gaggcccggg      300
40 agatcttcaa ggacgcggag aggacgaagc tgttctggat ttcttacagt gatggggacc     360
42 agtgtgcctc aagtcctatg cagaatgggg gctcctgcaa ggaccagctc cagtcctata     420
44 tctgcttctg cctccctgcc ttcgaggggc ggaactgtga gacgcacaag gatgaccagc     480
46 tgatctgtgt gaacgagaac ggcggctgtg agcagtactg cagtgaccac acgggcacca     540
48 agcgtcctct tcggtgccac gagggggtact ctctgctggc agacggggtg tcctgcacac     600
50 ccacagttga atatccatgt ggaaaaatac ctattctaga aaaaagaaat gccagcaaac     660
52 cccaaggcgc aattgtgggg ggcaagggtg gccccaaagg ggagtgtcca tggcaggtcc     720
54 tgttggttgt gaattgagct cagttgtgtg gggggaccct gatcaacacc atctgggtgg      780
56 tctccgcggc cactgtttc gacaaaatca agaactggag gaacctgatc gcggtgctgg      840
58 gcgagcacga cctcagcgag cagcaggggg atgagcagag ccggcgggtg gcgcaggtca     900
60 tcatccccag cacgtacgtc ccgggcacca ccaaccacga catcgcgctg ctccgcctgc     960
62 accagcccgt ggtcctcact gaccatgtgg tgcccctctg cctgcccga cggacgttct    1020
64 ctgagaggac gctggccttc gtgcgcttct cattggtcag cggtgggggc cagctgctgg    1080
66 accgtggcgc cagggccctg gagctcatgg tgetcaacgt gccccggtg atgaccagg    1140
68 actgcctgca gcagtcacgg aaggtgggag actcccaaaa taccacggag tacatgttct    1200
70 gtgcgggcta ctcggtggc agcaaggact cctgcaaggg ggacagtgga ggccacatg    1260
72 ccaccacta cgggggcacg tggtagctga cgggcatcgt cagctggggc cagggtgctg    1320
74 caaccgtggg ccactttggg gtgtacacca ggggtctcca gtacatcgag tggctgcaaa    1380
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79 <210> SEQ ID NO: 2

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80 &lt;211&gt; LENGTH: 466

81 &lt;212&gt; TYPE: PRT

82 &lt;213&gt; ORGANISM: Homo sapiens

84 &lt;400&gt; SEQUENCE: 2

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90 Gly Cys Leu Ala Ala Gly Gly Val Ala Lys Ala Ser Gly Gly Glu Thr
91          20          25          30
94 Arg Asp Met Pro Trp Lys Pro Gly Pro His Arg Val Phe Val Thr Gln
95          35          40          45
98 Glu Glu Ala His Gly Val Leu His Arg Arg Arg Arg Ala Asn Ala Phe
99          50          55          60
102 Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu
103 65          70          75          80
106 Gln Cys Ser Phe Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg
107          85          90          95
110 Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser
111          100          105          110
114 Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr
115          115          120          125
118 Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys Glu Thr His
119          130          135          140
122 Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly Cys Glu Gln
123 145          150          155          160
126 Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg Cys His Glu
127          165          170          175
130 Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro Thr Val Glu
131          180          185          190
134 Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys
135          195          200          205
138 Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys
139          210          215          220
142 Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly
143 225          230          235          240
146 Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His Cys Phe Asp
147          245          250          255
150 Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly Glu His Asp
151          260          265          270
154 Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val Ala Gln Val
155          275          280          285
158 Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp Ile Ala
159          290          295          300
162 Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro
163 305          310          315          320
166 Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val
167          325          330          335
170 Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala
171          340          345          350
174 Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu Met Thr Gln

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175          355          360          365
178 Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro Asn Ile Thr
179          370          375          380
182 Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys
183 385          390          395          400
186 Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg Gly Thr Trp
187          405          410          415
190 Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly
191          420          425          430
194 His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln
195          435          440          445
198 Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro
199          450          455          460
202 Phe Pro
203 465
206 <210> SEQ ID NO: 3
207 <211> LENGTH: 1401
208 <212> TYPE: DNA
209 <213> ORGANISM: Homo sapiens
211 <400> SEQUENCE: 3
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214 gcaggcgggg tcgctaaggc ctcaggagga gaaacacggg acatgccgtg gaagccgggg      120
216 cctcacagag tcttcgtaac ccaggaggaa gccacggcg tctgcaccg gcgccggcgc      180
218 gccaacgcgt tcttgaggga gctgcggccg ggctcccttg agagggagtg caaggaggag      240
220 cagtgtctct tcgaggaggc ccgggagatc ttcaaggacg cggagaggac gaagctgttc      300
222 tggatttctt acagtgatgg ggaccagtgt gcctcaagtc catgccagaa tgggggctcc      360
224 tgcaaggacc agctccagtc ctatatctgc ttctgcctcc ctgccttcga gggccggaac      420
226 tgtgagacgc acaaggatga ccagctgata tgtgtgaacg agaacggcgg ctgtgagcag      480
228 tactgcagtg accacacggg caccaagcgc tctgtcgggt gccacgaggg gtactctctg      540
230 ctggcagacg ggggtgtcctg cacaccaca gttgaatata catgtggaaa aatacctatt      600
232 ctagaaaaaa gaaatgccag caaaccccaa ggccgaattg tggggggcaa ggtgtgcccc      660
234 aaaggggagt gtccatggca ggtcctgttg ttggtgaatg gagctcagtt gtgtgggggg      720
236 accctgatca acaccatctg ggtgggtctcc gcggcccact gtttcgacaa aatcaagaac      780
238 tggaggaacc tgatcgcggt gctgggcgag caccagctca gcgagcacga cggggatgag      840
240 cagagccggc ggggtggcgca ggtcatcacc cccagcacgt acgtcccggg caccaccaac      900
242 caccacatcg cgctgctccg cctgcaccag cccgtgggtc tactgacca tgtggtgccc      960
244 ctctgcctgc ccgaacggac gttctctgag aggacgttg ccttcgtgcg cttctcattg     1020
246 gtcagcggct ggggccagct gctggaccgt ggcgccacgg ccctggagct catggtgctc     1080
248 aacgtgcccc ggctgatgac ccaggactgc ctgcagcagt cacggaaggt gggagactcc     1140
250 ccaaatatca cggagtacat gttctgtgcc ggctactcgg atggcagcaa ggactcctgc     1200
252 aagggggaca gtggaggccc acatgccacc cactaccggg gcacgtggta cctgacgggc     1260
254 atcgtcagct ggggccaggg ctgcgcaacc gtggggcact ttgggggtgta caccagggtc     1320
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258 ctgcgagccc catttcctta g                                     1401
261 <210> SEQ ID NO: 4
262 <211> LENGTH: 466
263 <212> TYPE: PRT
264 <213> ORGANISM: Homo sapiens
266 <400> SEQUENCE: 4

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268 Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
269 1      5      10      15
272 Gly Cys Leu Ala Ala Gly Gly Val Ala Lys Ala Ser Gly Gly Glu Thr
273      20      25      30
276 Arg Asp Met Pro Trp Lys Pro Gly Pro His Arg Val Phe Val Thr Gln
277      35      40      45
280 Glu Glu Ala His Gly Val Leu His Arg Arg Arg Arg Ala Asn Ala Phe
281      50      55      60
284 Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu
285 65      70      75      80
288 Gln Cys Ser Phe Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg
289      85      90      95
292 Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser
293      100     105     110
296 Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr
297      115     120     125
300 Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys Glu Thr His
301      130     135     140
304 Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly Cys Glu Gln
305 145     150     155     160
308 Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg Cys His Glu
309      165     170     175
312 Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro Thr Val Glu
313      180     185     190
316 Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys
317      195     200     205
320 Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys
321      210     215     220
324 Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly
325 225     230     235     240
328 Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His Cys Phe Asp
329      245     250     255
332 Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly Glu His Asp
333      260     265     270
336 Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val Ala Gln Val
337      275     280     285
340 Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp Ile Ala
341      290     295     300
344 Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro
345 305     310     315     320
348 Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val
349      325     330     335
352 Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala
353      340     345     350
356 Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu Met Thr Gln
357      355     360     365
360 Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro Asn Ile Thr
361      370     375     380
364 Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys

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365 385          390          395          400
368 Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg Gly Thr Trp
369          405          410          415
372 Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly
373          420          425          430
376 His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln
377          435          440          445
380 Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro
381          450          455          460
384 Phe Pro
385 465
388 <210> SEQ ID NO: 5
389 <211> LENGTH: 1335
390 <212> TYPE: DNA
391 <213> ORGANISM: Homo sapiens
393 <400> SEQUENCE: 5
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396 gcagtcttcg taaccaggga ggaagcccac ggcgtcctgc accggcgccg gcgcgccaac      120
398 gcgttcctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc      180
400 tccttcgagg agggccggga gatcttcaag gacgcggaga ggacgaagct gttctggatt      240
402 tcttacagtg atggggacca gtgtgcctca agtccatgcc agaatggggg ctcttgcaag      300
404 gaccagctcc agtctatat ctgcttctgc ctccctgcct tcgagggccg gaactgtgag      360
406 acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcggctgtga gcagtactgc      420
408 agtgaccaca cgggcaccaa gcgtcctgt cggtgccacg aggggtactc tctgctggca      480
410 gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa      540
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434 agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctccag      1260
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438 gcccatttc ctag      1335
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442 <211> LENGTH: 444
443 <212> TYPE: PRT
444 <213> ORGANISM: Homo sapiens
446 <400> SEQUENCE: 6
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453          20          25          30
456 Leu His Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro

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VERIFICATION SUMMARY

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